Phylogenetic Relationship of *Leymus chinensis* Revealed by the ITS and Chloroplast trnL-F Sequences

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Phylogenetic relationship of *Leymus chinensis* revealed by the ITS and chloroplast trnL-F sequences

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Key word : *Leymus chinensis* , *Psathyrostachys* , Xm genome , ITS , chloroplast trnL-F

Introduction Based on morphological observation , meiotic chromosome pairing of intergeneric hybrids , DNA hybridization patterns , and variation in repeated nucleotide sequences , previous studies have concluded that one genome in *Leymus* species originated from the genus *Psathyrostachys* (Wang *et al* , 2006) . Despite decades of intensive research , the precise phylogenetic relationship of *L* . chinensis is still unclear . The nuclear and chloroplast/mitochondrial sequences was used in many molecular phylogenetic studies for elucidating the origins and evolutionary history of polyploidy in plants , clarified their parental lineages . Particularly , internal transcribed spacers (ITS) and the intergenic spacer of trnL-trnF have been used widely in studying phylogenetic and genomic relationships of the diploid Poaceae genera . With additional abundant available sequences in public databases , ITS and trnL-trnF are the optimal choices in this study .

Materials and methods Two accessions of *L* . chinensis and *Psathyrostachys juncea* were included in this study . They were analyzed together with 18 related genera , consisting of 40 diploid species in the tribe Triticeae . *Bromus catharticus* was used as the outgroup based on previous phylogenetic studies . The aligned data set of the ITS and the *trnL-F* were analyzed using PAUP version 4 .0 . Heuristic search was implemented with 100 random additional sequence replicates , tree-bisection-reconnection (TBR) branch swapping , MULPARS option , and ACCTRAN optimization . To evaluate relative robustness of the clades found in the most parsimonious trees , bootstrap analysis was conducted using 500 replicates with a simple taxon addition .

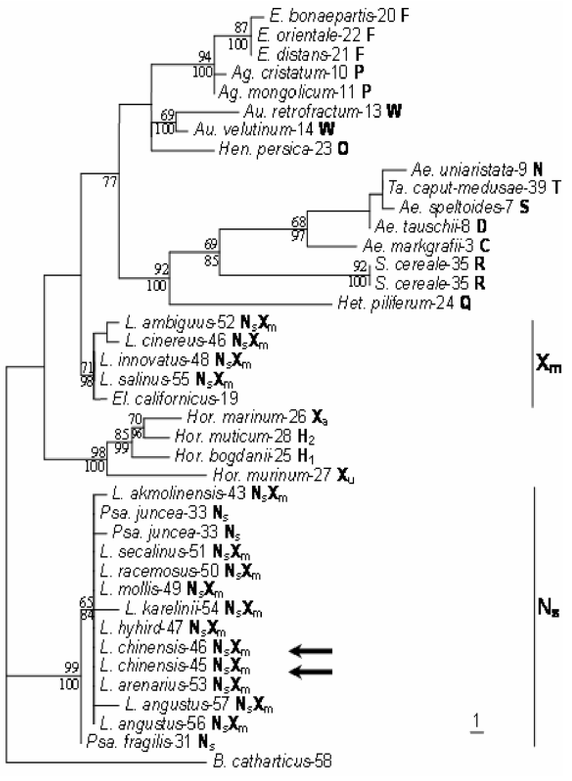

Figure 1 *One of the 500 most parsimonious (MP) trees generated from the* trnL-F *sequences (Tree length = 147 , CI = 0 .7687 , RI = 0 .8707) . The topologies obtained by Bayesian analysis are identical except for some nodes having different bootstrap values .*

Results It was showed that : (1) The ITS sequences revealed polyploidy *Leymus* have close phylogenic relationships with *Psathyrostachys* and an unknown genus in Triticeae . The ITS tree suggested considerable differentiation among *Leymus* species and recurrent hybridization of *Leymus* . (2) The trnL-F tree revealed especially close relationships of partial *Leymus* species and *Psathyrostachys* , residual *Leymus* species and an unknown genus (Figure 1) . The trnL-F tree showed that the mother of *Leymus chinensis* was *Psathyrostachys* , and the father was the Xm genome .

Conclusions The results indicated that it was unlikely that the unknown genome in *Leymus* species originated from a modified version of the Ns genome or any sampled diploid species in present study ; The maternal of *L* . chinensis was Ns genome and the paternal genome was Xm .

Reference

Wang RRC , Zhang JY , Lee BS , Jensen KB , Kishii M , Tsujimoto H (2006) . Variations in abundance of 2 repetitive sequences in *Leymus* and *Psathyrostachys* species . *Genome* , 49 , 511-519 .